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Figure 1a

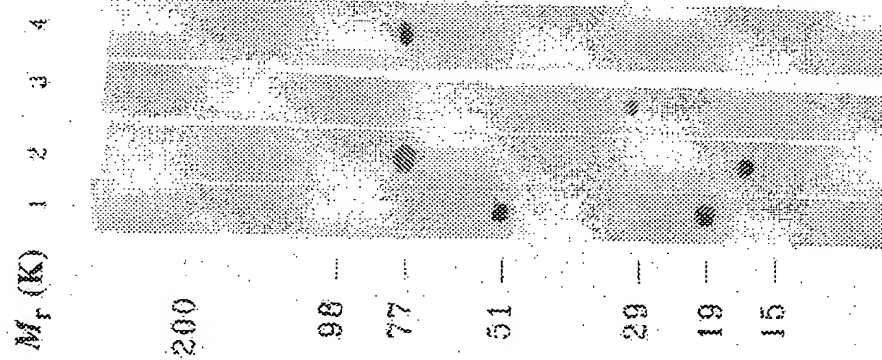
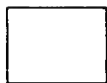
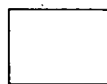
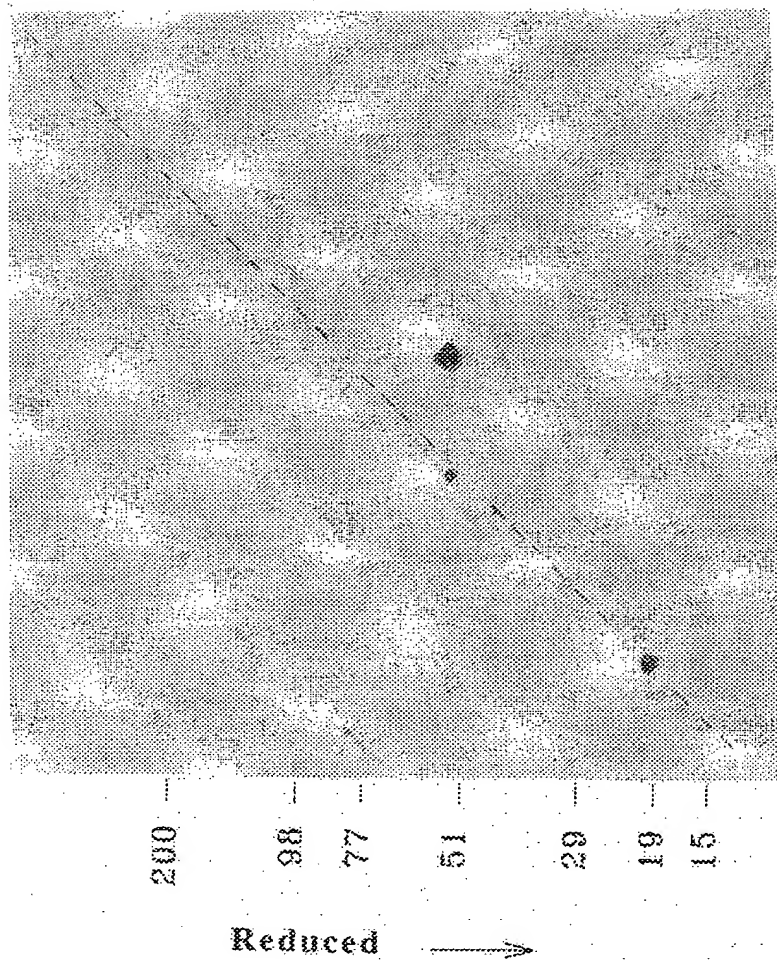


Figure 1b

← Non-reduced

15 19 29 51 77 98 200 M_r (K)





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Figure 2

— C1r/C1s —>

MASP-2 TPLGPKWPEPVFGRLASPGFPGGEYANDQERRWTLTAPPGYRLRLYFTHFDELSHLCEYDFVKLSSGAKVLATLEGEESTDTERAPGKDT 90

MASP-1 HTVELNNMFGQIQSPGYPDSYPSDSEVTWNITVPDGFRIKLYFMHFNLESSYLCEYDYVKVETEDQVLATFGRETTDTEQTPGQEV 87

C1r SIPIPKQLFGEVTSPLFPKPYFNNFETTTTITVPTGYRVKLVFQPPDLEPSEGCFYDYVKISADKKSRLGRFGQLGSGPLGNPPGKKE 87

C1s EPTMYGEILSPNYPQAYPSEVEKSWDIEVPEGYGIHLYFTHLDIELSENCAYSVQIISGDTEEGRLCGQRSSNNPHSPIVEE 83

* * * * *

EGF —>

MASP-2 FYSLGSSLDITFRSDYSNEKP FTGFEAFYAARDIDEQ VAPGEA PTCDDHCHNHLGGFYCSRAGYVLHRNKRTCSALCS 170

MASP-1 VLSPGSFMSTITFRSDFSNEER FTGFDAYHMAVDVDECK EREDEE LSCDHYCHNYIGGYCSRFGYILHTDNRTSRVECS 167

C1r FMSQGNKMLLTFTDFSNENGTIMFYKGLLAYQAVDLDEASRSKSGEEDPOPCQHLCHNYVGGYFCSRPGYELQEDRHSQAECS 177

C1s FQVPYNKLQVIFKSDFSNEER FTGFAAYVATDINEET DFVD VPESHFONNFIGGYFCSPPPEYFLHDDMKNGVNES 161

* * * * *

— C1r/C1s —>

MASP-2 GQVFTQSGELSSPEYPRPYKLSSTYSSISLEEGFSVILDFV ESFDVET HPETLCFYPDFLKIQTDRREEHGPFGKTLPHR IETKS 256

MASP-1 DNLFTQRTGVITSPDPFPNYPYKSSSEQLYTIELEEGFMVNLOFE DIFDIED HPEVPPPYDYIKIKVGPVKLGPPGGEKAPPEP ISTQS 253

C1r SELYTEASGYISSLEYPRSYPPDLRCNYSIRVERGLTLHLKFL EPFDIDD HQQVHPYDQLQIYANGKNIGEFQKQRPDP LDTSS 263

C1s GDVFTALIGEIASPNYPKYPENSRCYQIRLEKGFQVVTLRREDFDVEAADSAGN LDSLVFVAGDRQFGPYCGHGFPGPLNIETKS 250

* * * * *

CCP-1 —>

MASP-2 NTVTITFVTDESGDHTGWKIHYTSTAQPCPYPMAPPN GHVSPVQAKYILKDSFSIFMETGYELLQHLPLKSFTAVCQKDGSDWRPMPA 345

MASP-1 HSVLILFHSNDNGENRGWRLSYRAAGNEPELOPPVH GKIEPSQAKYFFKDQVLVSQDTGYKVLKDNVEMDTFQIECLKDGTWSNKIPT 342

C1r NAVDLLFTDESGDSRGWKLRYTTEIIKQPPKTLDEFTIIQNLQPYQFRDYFIATCKQGYQLIEGNQVLSFTAVCQDDGTWHRAMPR 353

C1s NALDIIPTQDLTGQKKGWKLRYHGDPMPCPKEDTPN SVWEPKAKYVFRDVVQITCLDGFVVEGRVAGTSFYSTCQSNKGWSNKLK 338

* * * * *

CCP-2 —>

MASP-2 CSIVDCGPPDDLPSGRVEYITGPGVTTYKAVIQYSCBETFYTM KVNDGKYVCEADGFWTSSKGEKSLPVECPVCGLS ARTT 426

MASP-1 CKIVDCRAPGELEHGLITFSTRNNLTYYKSEIKYSQEPYKML NNTNGIYTCQAQGVWMNKVLRSLPTCLPVEGLPKFSRKL 426

C1r CKIKDCQPRNLNPGDFRYTTTGMVNTYKARIQYCHEPYKMQTRAGSRESEQGVYTCTAQGIWKNQKQEKIPRELPGVCKPVPNPVEQ 443

C1s CQPVDCGIPESIENGKVE DPESTLFGSVIRYTCBEPYYME NGGGGEYHCAGNGSWVNEVLGPPLPKCPVPCGVPREPFEE 419

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serine protease —>

MASP-2 GGRIYGGQKAKPGDFPWQVLILGTTA AGALLYDNWVLTAAH AVYEQKHDSALDIRMGTLRKLSPHYTQAWSEAVFIHEG 507

MASP-1 MARIFNGRPAQKGTTPWIAMLSHLNGQPFCCGSSLLGSSWIVTAAHCLHQSLDPKPTLRSDLLSPSD FKIIILGKHWRLRSDENEQHLG 515

C1r RQRIIGGQKAKMGNFPWQVFTNIHGRG GGALLGDRWILTAAH TLYPKEHAQSNASLDVFLGHTNVVEELMKLGNHP IRRV 523

C1s KQRIIGGSADIKNFPWQVFFDNPA GGALINEYVLTAAH VVEGNREPTMYGVSTSVQTSRLAKSKMLT PEHVFIHPG 498

* * * * *

YTHDAG

MASP-2 YTHDAG FDNIDIALIKLNNKVINSNITPICLPRKEAESFMRTDDIGTASGWGLTQRGFLARNLAMYVDIPIVDHQAATAAYEK 589

MASP-1 VKHTTLHPKYDPNTFENDVALVELLESPVLNAFVMPICLP EGPOQEGAMVIVSGWGKQLQRFPELMEIEIPIVDHSTQOKAY 599

C1r SVHPDYRQDESYN PEGDIALLELENSVTLPNLLPICLP DNDTFYDLGLMGYVSGFGVMEEK IAHDLRFVRLPVPANPQAHEN WLR 608

C1s WKLLV PEGRTN FDNIDIALVRLKDPVKMGPTVSPICLPPTSSDYNLMDGLGLISGWGRTEKRDRAVRLKAARLPVAPLRKKEVKVE 586

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PPYPRG

MASP-2 PPYPRG SVTANMLCAGLES GGKDSERGDSSGALVFLDS ETERWFVGGIVSWGSMNCGEAGQYGVYTKVINIYIPWIENIISDF 671

MASP-1 APLKK KVTRDMICAGEKEGGKDAESGDSGGPMVTLNR ERGQWYLVGTVSWG DGGKDRYGVVSYIHNKNDWIQRTVGVNR 680

C1r GKNRMD VFSQNMFCAGHPSLKQDAQOGDSGGVFAVRDP NTRDWATGIVSWG GDSRG YGFTYKVLNVYDVIKKEMEED 688

C1s KPTADAEAYFTPNMICAGGEK GMDSCKGDSSGAFVQDPNDKTFYAGLVSWG QCGT YGLYTRVQNVYDVIKMTMQENSTPRED 673

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Figure 3a

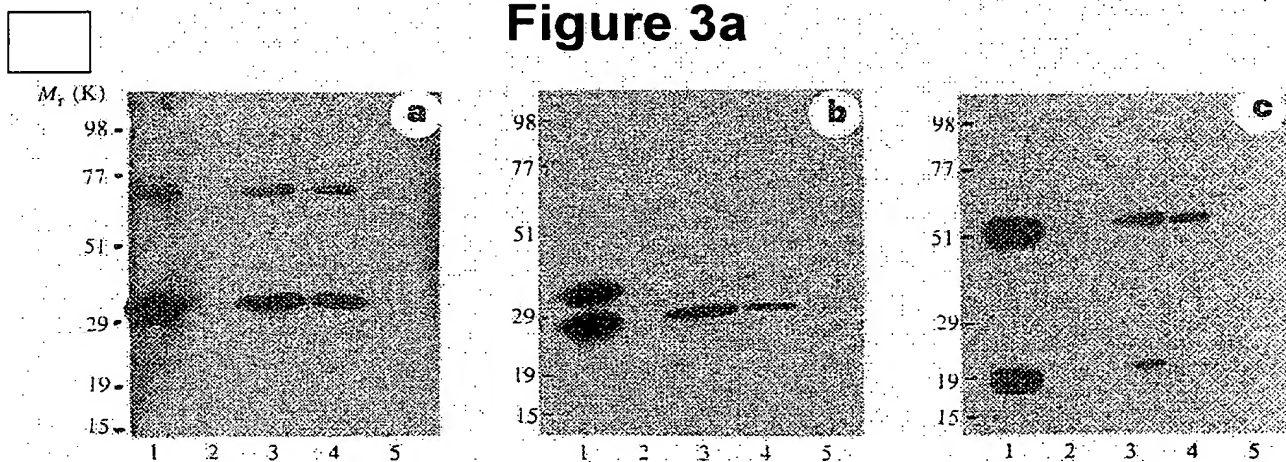
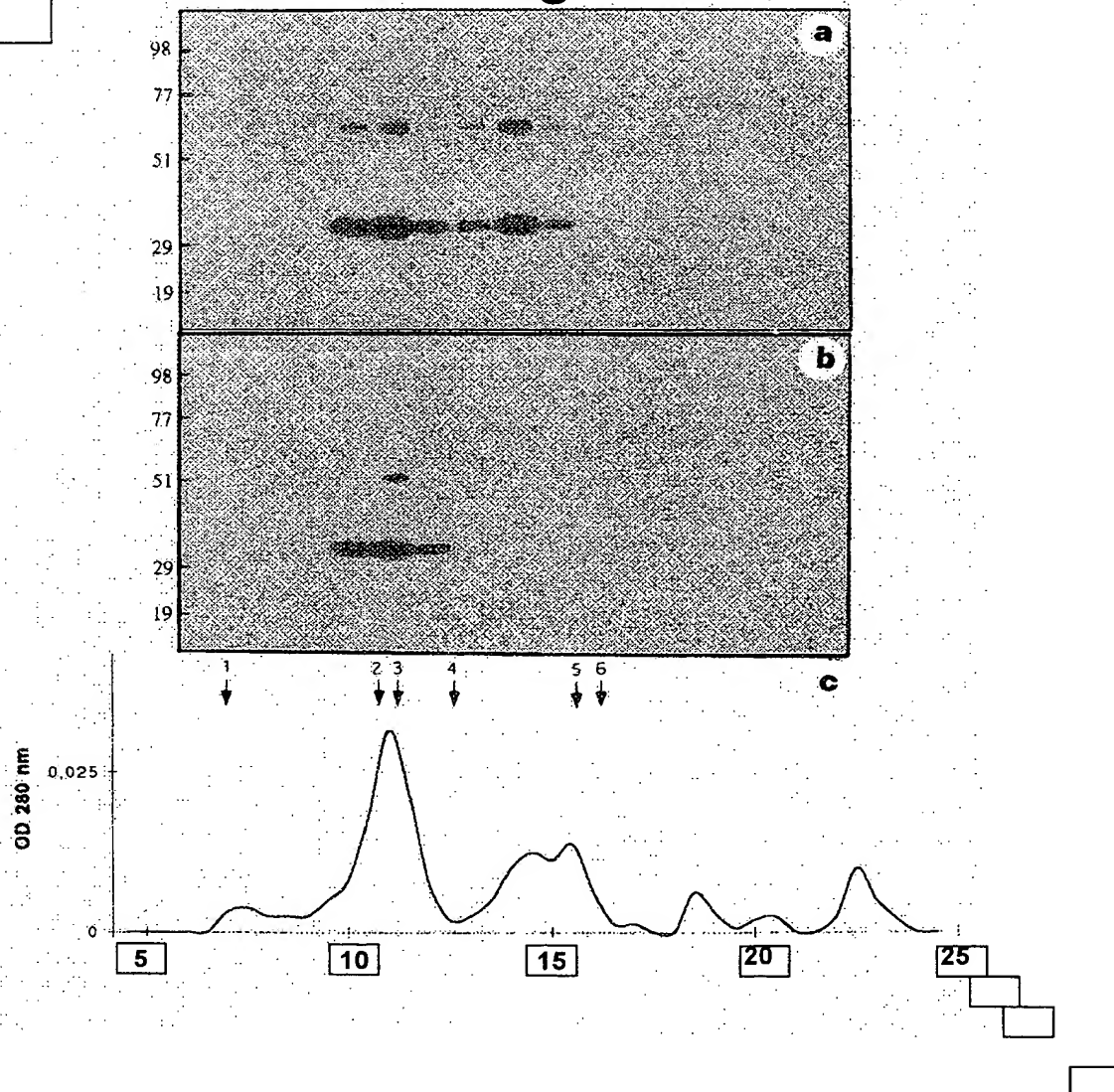
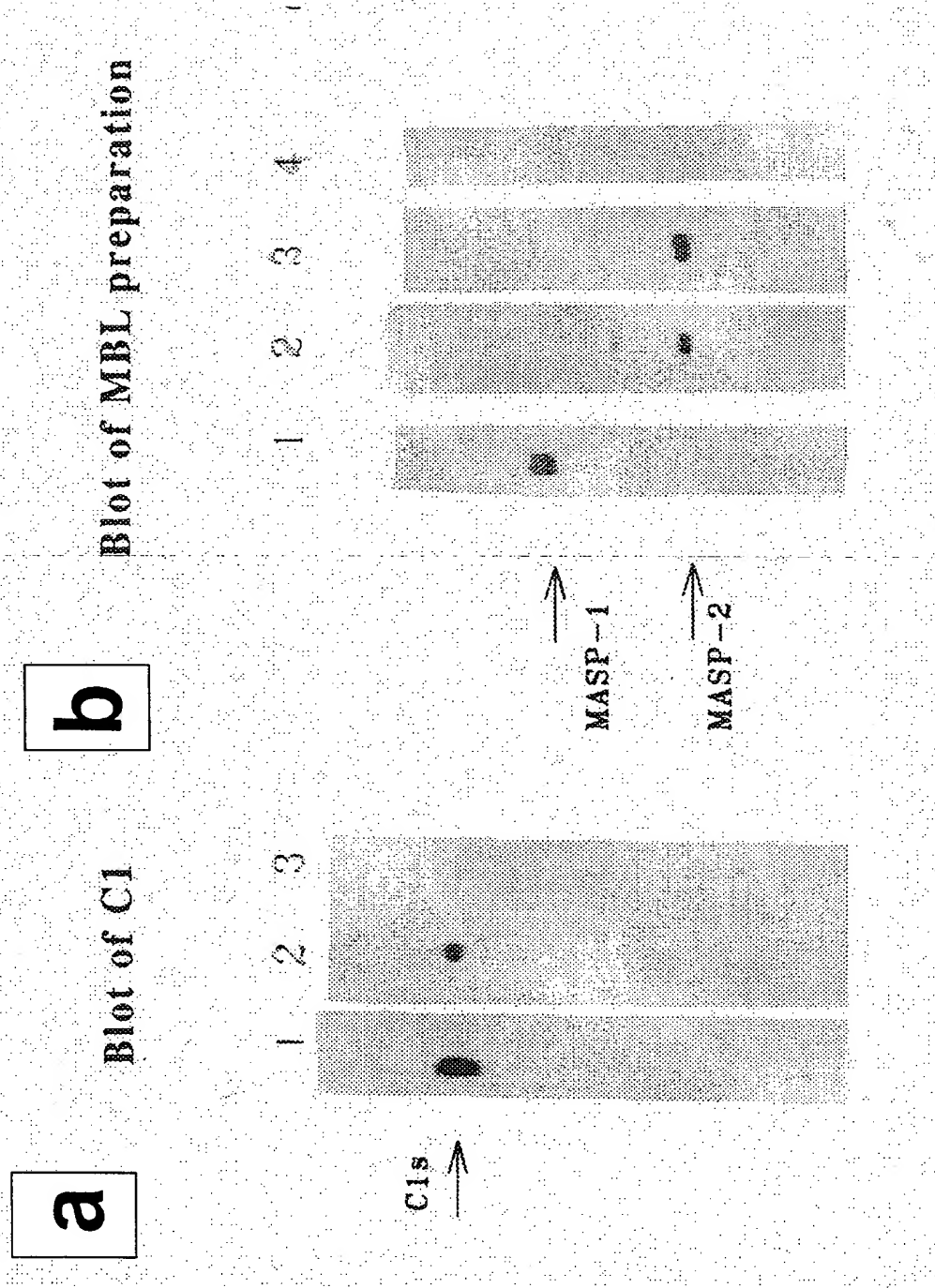


Figure 3b



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Figure 4



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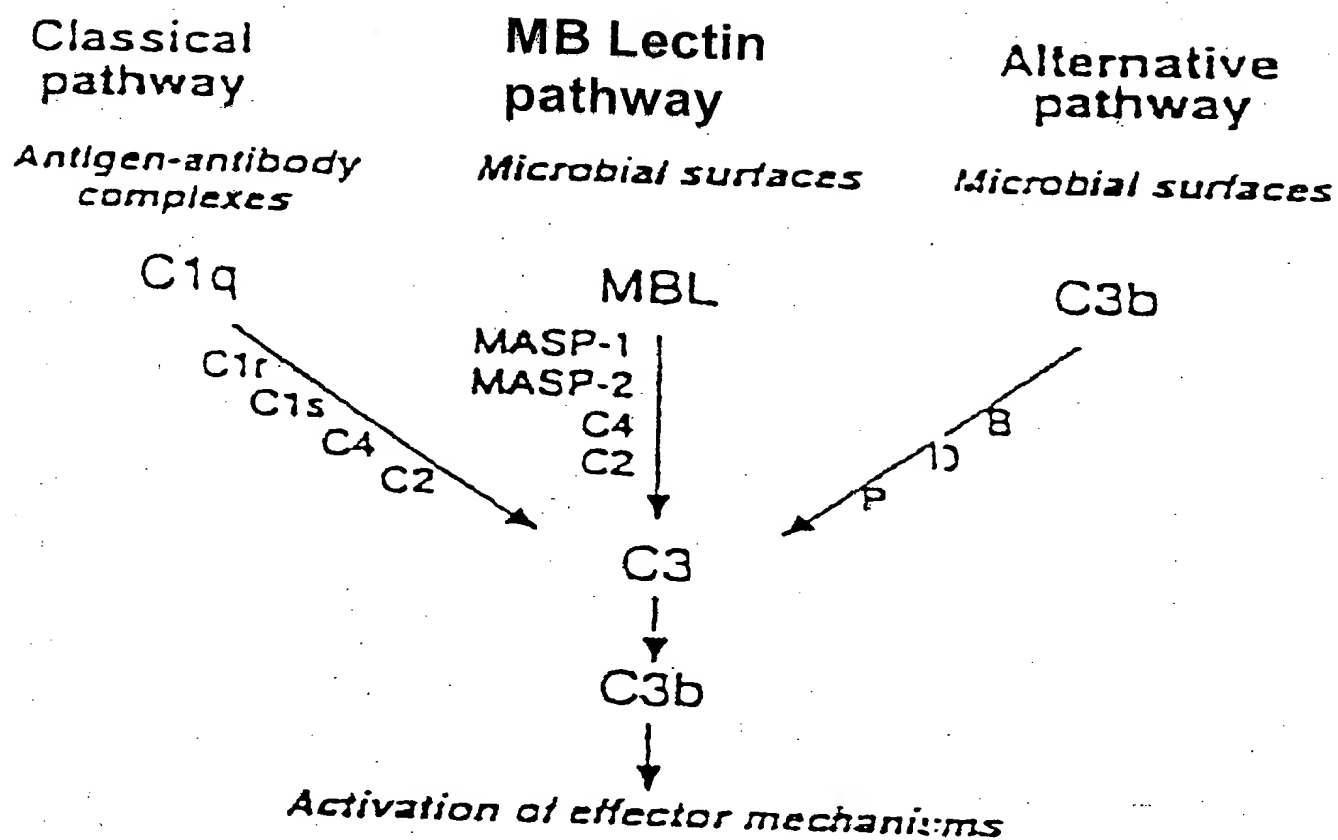


Figure 5

